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DEC 06 2002

TECH CENTER 1600/2900

1	AGCAGACAGAGGACTCTCATTAAAGGAAGG TGTCCTGTGCCCTGACCCCTACAAGATGCCA	59
	Met Pro	2
60	AGAGAAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGCACGGCCACTCTTACACC	119
3	Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly His Gly His Ser Tyr Thr	22
120	ACGGCTGAAGAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC	179
23	Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu	42
180	ATCGGCTGTTGGTATTGTAGAAAGACGAAAT GGATACAGAGCCCTTGATGGATAAAAGTCTT	239
43	Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu	62
240	CATGTTGGCACTCAATGTGCCCTTAACAAGA AGATGCCCCACAAGAAAGGGTTTGATCATCGG	299
63	His Val Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg	82
300	GACAGCAAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCTCCCAATGCTCCACCT	359
83	Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro Asn Ala Pro	102
360	GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG	419
103	Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser Pro Pro Tyr Ser Pro	118
420	AGACACCTGAGACATGCTGAAATATTCTCT CTCACACTTTTGCTTGAATTAAATACAGAC	479
480	ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC	539
540	AGTGTTAAATTTTAGTAGGTCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA	599
600	TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA	659

FIG. 1



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660 GGTAATGTTAGTAAATCCATGGTGTATTT TCTGAGAGACAGAAATTCAGTGGGTATCT 719  
720 GGGGCCATCCAAATTTCTTTACTTTGAAAT TTGGCTAATAACAACACTAGTCAGGTTTTTCG 779  
780 AACCTTGACCGACATGAACGTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG 839  
840 GATACTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT 899  
900 CAGCAATGTCTCTTTGTGCTCTAAAAATTCT ATTATACTACAATAATATATTGTAAAGATC 959  
960 CTATAGCTCTTTTTTTTGTGAGATGGAGTTT CGCTTTTGTGCCCCAGGCTGGAGTGCAATG 1019  
1020 GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCCTTAG 1079  
1080 CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTT 1139  
1140 AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA 1199  
1200 TCTGCCCCCTCAGCCTCCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCCACGCTGGCT 1259  
1260 GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACCTTCAAGGCTC 1319  
1320 AATGCTATTCTAACTAATGACAAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT 1379  
1380 AAATAAGTAAAGCTACTATGTACTGCCCTT AGTGCTGATGCCCTGTGTACTGCCCTTAAATG 1439  
1440 TACCTATGGCAATTTAGCTCTCTTGGGTTT CCAAATCCCTCTCACAAAGAAATGTGCAGAAG 1499  
1500 AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIG. 1 Continued

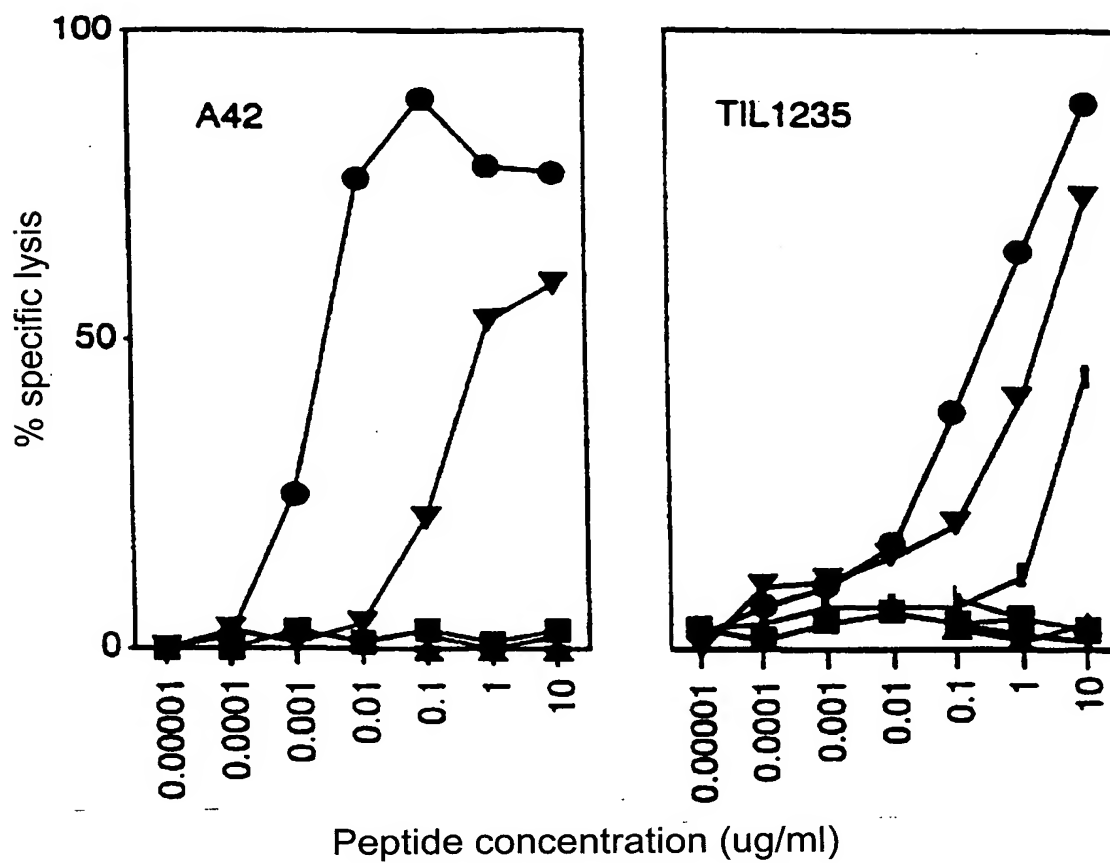


FIG. 2



In re Appln. of Kawakami et al.  
U.S. Patent Appln. No. 09/073,138  
Art Unit: 1642  
Confirmation No. 7367  
Docket No. 218757  
Sheet 4 of 9

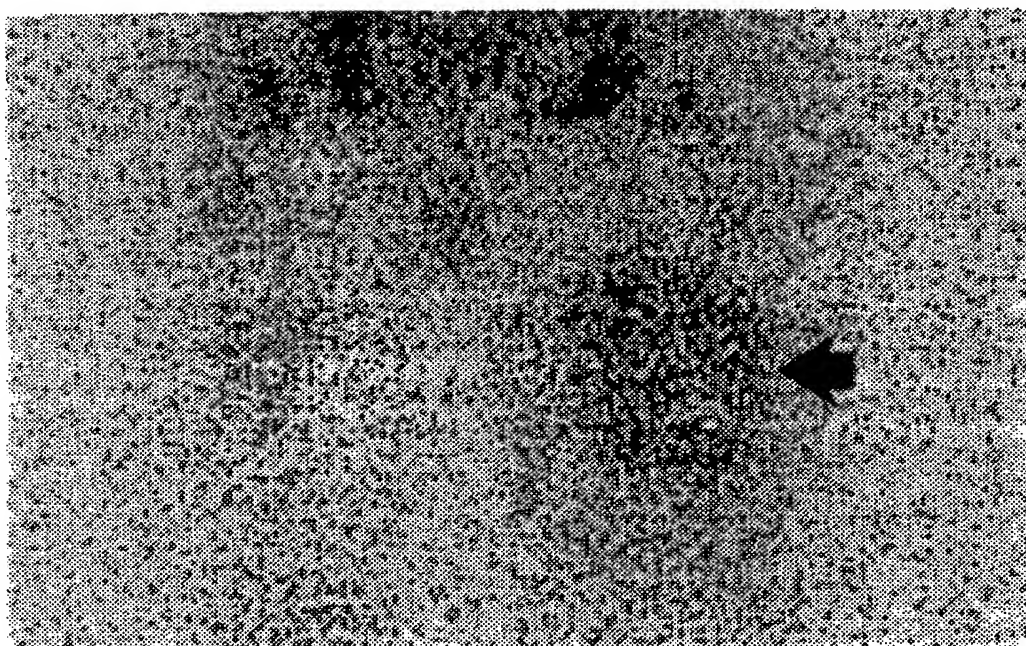


FIG. 3A

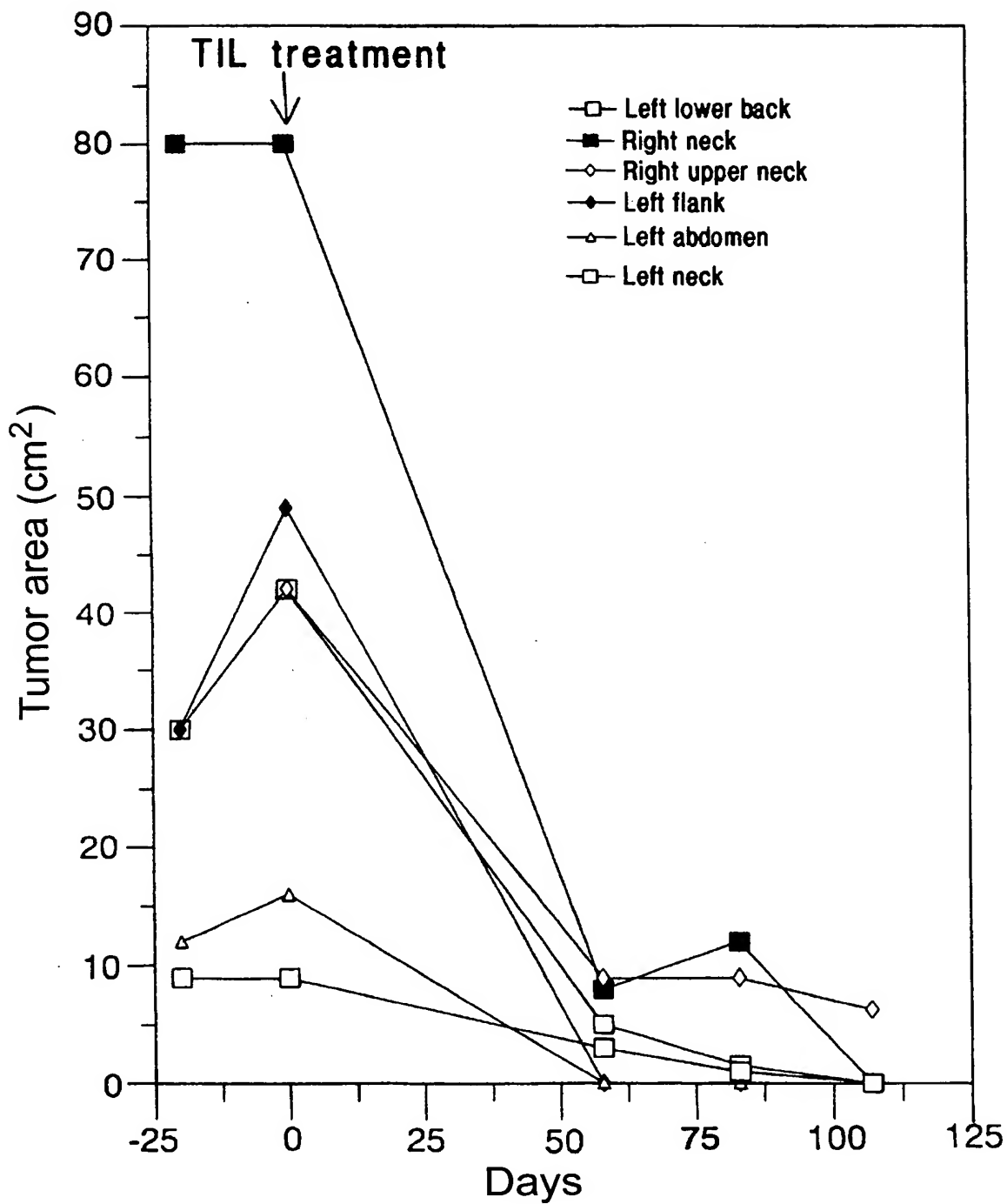


FIG. 3B



GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGA CTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIG. 4



TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACCTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIG. 4 (Continued)



1	MDLVLRCLL	HLAVIGALLA	VGATKVPNRQ	DWLGVSRLR	TKAWNRLYP
51	EWTEAQRDC	WRGGQVSLKV	SNDGPTLIGA	NASFSLALNF	PGSQKVLDPG
101	QVIWVNTII	NGSQVWGGQP	VYPQETDDAC	IFPDGGPCPS	GSWSQKRSFV
151	YVWKTWGQYW	QFLGGPVSGL	SIGTGRAMLG	THIMEVTVYH	RRGSRSYVPL
201	AHSSSAFTIT	DQVPFSVSVS	QLRALDGGNK	HFLRNQPLTF	ALQLHDPSGY
251	LAEADLSYTW	DFGDSSGTLI	SRALVVTHTY	LEPGPVTAQV	VLQAAIPLTS
301	CGSSPVPGETT	DGHRPTAEAP	NTTAGQVPTT	EVVGTTPGQA	PTAEPSTGTS
351	VQVPTTEVIS	TAPVQMPTAE	STGMTPEKVP	VSEVMGTTLA	EMSTPEATGM
401	TPAEVSIVVL	SGTTAAQVTT	TEWVETTARE	LPIPEPEGPD	ASSIMSTESI
451	TGSLGPLLDG	TATLRLVKRQ	VPLDCVLYRY	GSFSVTLDIV	QGIESAEILQ
501	AVPSGEGDAF	ELTVSCQGGL	PKEACMEISS	PGCOPPAQRL	CQFVLPSFAC
551	QLVLHQILKG	GSPTYCLNVS	LADTNSLAVV	STQLIMPGQE	AGLGQVPLIV
601	GILLVLMVVV	LASLIYRRRL	MKQDFSVPQL	PHSSSHWLRL	PRIFCSCPIG
651	ENSPLLSGQQ	V			

FIG. 5A

Pme117	M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20	M-----V-----Q-----L-----
gp100	M-----V-----Q-----L-----
CDNA25FL	M-----F-----Q-----L-----
CDNA25TR	Q-----L-----PPQWAAGLSTLI
	1      162      236      274      588      649

FIG. 5B

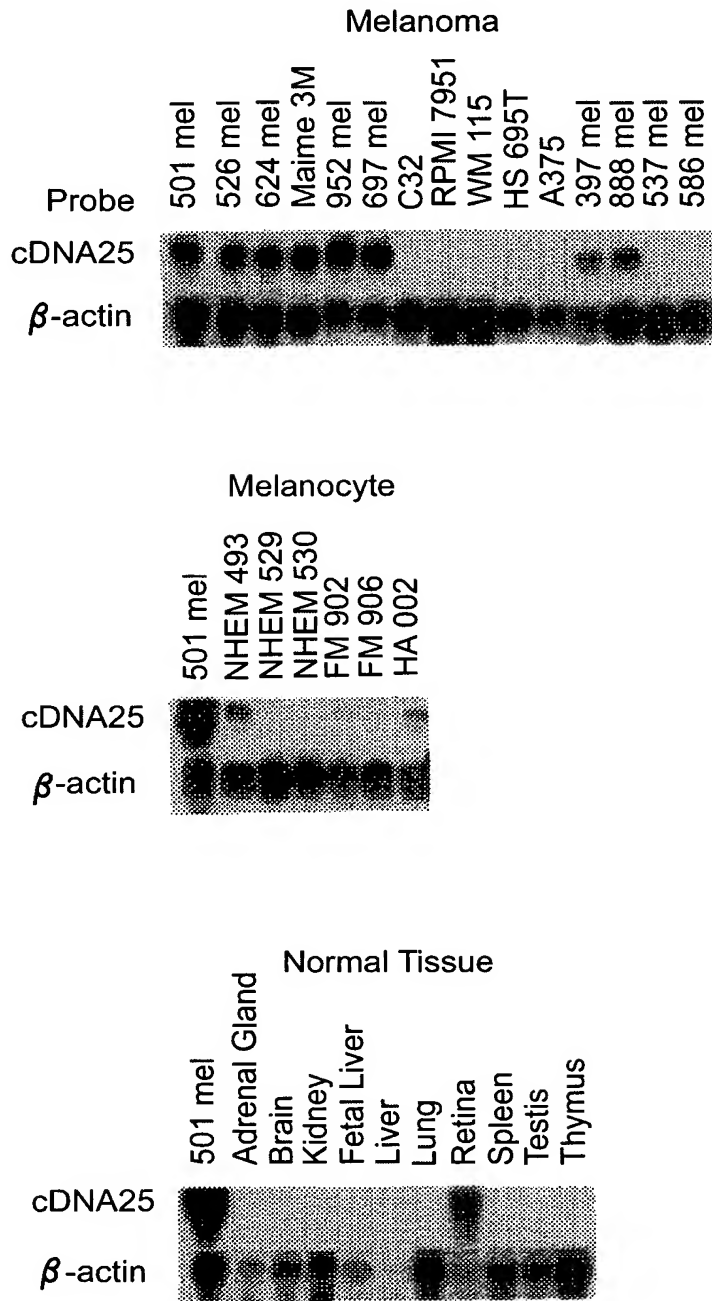


FIG. 6